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**RAW SEQUENCE LISTING
PATENT APPLICATION US/08/422,548**

TEAM 6

ESCUELA CS
DATE: 07/11/95
TIME: 09:23:37

INPUT SET: S4668

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: Eaton, Dan L.
6 DeSauvage, Frederic J.
7
8 (ii) TITLE OF INVENTION: MPL LIGAND
9
10 (iii) NUMBER OF SEQUENCES: 32
11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: Genentech, Inc.
14 (B) STREET: 460 Point San Bruno Blvd
15 (C) CITY: South San Francisco
16 (D) STATE: California
17 (E) COUNTRY: USA
18 (F) ZIP: 94080
19
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: 5.25 inch, 360 Kb floppy
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: patin (Genentech)
25
26 (vi) CURRENT APPLICATION DATA:
27 (A) APPLICATION NUMBER:
28 (B) FILING DATE: 13-APR-1995
29 (C) CLASSIFICATION:
30
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: 08/223263
33 (B) FILING DATE: 04-APR-1994
34
35 (vii) PRIOR APPLICATION DATA:
36 (A) APPLICATION NUMBER: 08/196689
37 (B) FILING DATE: 15-FEB-1994
38
39 (vii) PRIOR APPLICATION DATA:
40 (A) APPLICATION NUMBER: 08/185607
41 (B) FILING DATE: 21-JAN-1994
42
43 (vii) PRIOR APPLICATION DATA:
44 (A) APPLICATION NUMBER: 08/176553
45 (B) FILING DATE: 03-JAN-1994
46

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47 (viii) ATTORNEY/AGENT INFORMATION:
48 (A) NAME: Winter, Daryl B.
49 (B) REGISTRATION NUMBER: 32,637
50 (C) REFERENCE/DOCKET NUMBER: 871P3D1

51
52 (ix) TELECOMMUNICATION INFORMATION:
53 (A) TELEPHONE: 415/225-1249
54 (B) TELEFAX: 415/952-9881
55 (C) TELEX: 910/371-7168

56
57 (2) INFORMATION FOR SEQ ID NO:1:

58
59 (i) SEQUENCE CHARACTERISTICS:
60 (A) LENGTH: 353 amino acids
61 (B) TYPE: amino acid
62 (D) TOPOLOGY: linear

63
64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

65 Met Glu Leu Thr Glu Leu Leu Leu Val Val Met Leu Leu Leu Thr
66 1 5 10 15
67
68 Ala Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu
69 20 25 30
70
71 Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser
72 35 40 45
73
74 Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val
75 50 55 60
76
77 Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln
78 65 70 75
79
80 Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu
81 80 85 90
82
83 Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr
84 95 100 105
85
86 Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu
87 110 115 120
88
89 Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro
90 125 130 135
91
92 Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu
93 140 145 150
94
95 Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu
96 155 160 165
97
98 Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr
99

**RAW SEQUENCE LISTING
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100	170	175	180
101			
102	Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu		
103	185	190	195
104			
105	Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser		
106	200	205	210
107			
108	Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe		
109	215	220	225
110			
111	Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu		
112	230	235	240
113			
114	Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn		
115	245	250	255
116			
117	Gly Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly		
118	260	265	270
119			
120	Ala Pro Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro		
121	275	280	285
122			
123	Pro Asn Leu Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro		
124	290	295	300
125			
126	Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr		
127	305	310	315
128			
129	Pro Val Val Gln Leu His Pro Leu Leu Pro Asp Pro Ser Ala Pro		
130	320	325	330
131			
132	Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser Tyr Thr His		
133	335	340	345
134			
135	Ser Gln Asn Leu Ser Gln Glu Gly		
136	350	353	
137			
138	(2) INFORMATION FOR SEQ ID NO:2:		
139			
140	(i) SEQUENCE CHARACTERISTICS:		
141	(A) LENGTH: 1795 bases		
142	(B) TYPE: nucleic acid		
143	(C) STRANDEDNESS: single		
144	(D) TOPOLOGY: linear		
145			
146	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:		
147			
148			
149	TCTTCCTACC CATCTGCTCC CCAGAGGGCT GCCTGCTGTG CACTTGGGTC 50		
150			
151			
152	CTGGAGCCCT TCTCCACCCG GATAGATTCC TCACCCCTGG CCCGCCTTG 100		

**RAW SEQUENCE LISTING
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153
154
155 CCCCCACCCTA CTCTGCCAG AAGTGCAAGA GCCTAAGCCG CCTCCATGGC 150
156
157
158 CCCAGGAAGG ATTCAGGGGA GAGGCCCCAA ACAGGGAGCC ACGCCAGCCA 200
159
160
161 GACACCCCGG CCAGAATGGA GCTGACTGAA TTGCTCCTCG TGGTCATGCT 250
162
163
164 TCTCCTAACT GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG 300
165
166
167 ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC 350
168
169
170 AGACTGAGCC AGTCCCCAGA GGTTCACCCCT TTGCCTACAC CTGTCCTGCT 400
171
172
173 GCCTGCTGTG GACTTTAGCT TGGGAGAATG GAAAACCCAG ATGGAGGAGA 450
174
175
176 CCAAGGCACA GGACATTCTG GGAGCAGTGA CCCTTCTGCT GGAGGGAGTG 500
177
178
179 ATGGCAGCAC GGGGACAACG GGGACCCACT TGCTCCTCAT CCCTCCTGGG 550
180
181
182 GCAGCTTTCT GGACAGGTCC GTCTCCTCCT TGGGGCCCTG CAGAGCCTCC 600
183
184
185 TTGGAACCCA GCTTCCTCCA CAGGGCAGGA CCACAGCTCA CAAGGATCCC 650
186
187
188 AATGCCATCT TCCTGAGCTT CCAACACCTG CTCCGAGGAA AGGTGCCTTT 700
189
190
191 CCTGATGCTT GTAGGAGGGT CCACCCCTCTG CGTCAGGCAG GCCCCACCCA 750
192
193
194 CCACAGCTGT CCCCCAGCAGA ACCTCTCTAG TCCTCACACT GAACGAGCTC 800
195
196
197 CCAAACAGGA CTTCTGGATT GTTGGAGACA AACTTCACTG CCTCAGCCAG 850
198
199
200 AACTACTGGC TCTGGCTTC TGAAGTGGCA GCAGGGATTC AGAGCCAAGA 900
201
202
203 TTCCTGGTCT GCTGAACCAA ACCTCCAGGT CCCTGGACCA AATCCCCGGA 950
204
205

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206 TACCTGAACA GGATACACGA ACTCTTGAAT GGAACCTCGTG GACTCTTC 1000
207
208
209 TGGACCCTCA CGCAGGACCC TAGGAGCCCC GGACATTCC TCAGGAACAT 1050
210
211
212 CAGACACAGG CTCCCTGCCA CCCAACCTCC AGCCTGGATA TTCTCCTTCC 1100
213
214
215 CCAACCCATC CTCCTACTGG ACAGTATAACG CTCTTCCCTC TTCCACCCAC 1150
216
217
218 CTTGCCACC CCTGTGGTCC AGCTCCACCC CCTGCTTCCT GACCCTCTG 1200
219
220
221 CTCCAACGCC CACCCCTACC AGCCCTCTTC TAAACACATC CTACACCCAC 1250
222
223
224 TCCCAGAACATC TGTCTCAGGA AGGGTAAGGT TCTCAGACAC TGCCGACATC 1300
225
226
227 AGCATTGTCT CATGTACAGC TCCCTTCCCT GCAGGGCGCC CCTGGGAGAC 1350
228
229
230 AACTGGACAA GATTCCTAC TTTCTCCTGA AACCCAAAGC CCTGGTAAAA 1400
231
232
233 GGGATACACA GGACTGAAAA GGGAAATCATT TTTCACTGTA CATTATAAAC 1450
234
235
236 CTTCAGAAC TATTTTTTA AGCTATCAGC AATACTCATC AGAGCAGCTA 1500
237
238
239 GCTCTTGGT CTATTTCTG CAGAAATTTG CAACTCACTG ATTCTCTACA 1550
240
241
242 TGCTCTTTT CTGTGATAAC TCTGCAAAGG CCTGGGCTGG CCTGGCAGTT 1600
243
244
245 GAACAGAGGG AGAGACTAAC CTTGAGTCAG AAAACAGAGA AAGGGTAATT 1650
246
247
248 TCCTTTGCTT CAAATTCAAG GCCTTCCAAC GCCCCCACCC CCTTTACTAT 1700
249
250
251 CATTCTCACT GGGACTCTGA TCCCATATTG TTAACAGATC TTTACTCTTG 1750
252
253
254 AGAAATGAAT AAGCTTCTC TCAGAAAAAA AAAAAAAAAA AAAAAA 1795
255
256
257
258 (2) INFORMATION FOR SEQ ID NO:3:

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION **US/08/422,548**

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Error

Original Text